#7

<111> Goldsmith, Elizabeth J.
Radha, Akella
Gaynor, Richard B.

<120> CHIMERIZING PROTEIN KINASES FOR DRUG DISCOVERY

<130> A33864 090495.0232

<140> 09/918,873
<141> 2001-07-31

<160> 39

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 360
<212> PRT
<213> Rattus norvegicus

<400> 1

```
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His
65                  70                  75                  80
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
```

```
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro
            340                 345                 350
Leu Asp Gln Glu Glu Met Glu Ser
        355                 360


<210> 2
<211> 379
<212> PRT
<213> Rattus norvegicus

<308> AAF21978
<309> 2001-01-01

<400> 2
Met Ser Trp Ser Pro Ser Leu Pro Thr Gln Thr Cys Gly Ala Trp Glu
 1               5                  10                  15
Met Lys Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Ile Arg Trp
            20                  25                  30
His Asn Gln Val Thr Gly Glu Gln Ile Ala Ile Lys Gln Cys Arg Gln
        35                  40                  45
Glu Leu Ser Pro Lys Asn Arg Asp Arg Trp Cys Leu Glu Ile Gln Ile
    50                  55                  60
Met Arg Arg Leu Asn His Pro Asn Val Val Ala Ala Arg Asp Val Pro
65                  70                  75                  80
Glu Gly Met Gln Asn Leu Ala Pro Asn Asp Leu Pro Leu Leu Ala Met
                85                  90                  95
Glu Tyr Cys Gln Gly Gly Asp Leu Arg Arg Tyr Leu Asn Gln Phe Glu
            100                 105                 110
Asn Cys Cys Gly Leu Arg Glu Gly Ala Ile Leu Thr Leu Leu Ser Asp
        115                 120                 125
Ile Ala Ser Ala Leu Arg Tyr Leu His Glu Asn Arg Ile Ile His Arg
    130                 135                 140
Asp Leu Lys Pro Glu Asn Ile Val Leu Gln Gln Gly Glu Lys Arg Leu
145                 150                 155                 160
Ile His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Glu Leu Asp Gln Gly
                165                 170                 175
Ser Leu Cys Thr Ser Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu
            180                 185                 190
Leu Leu Glu Gln Gln Lys Tyr Thr Val Thr Val Asp Tyr Trp Ser Phe
        195                 200                 205
Gly Thr Leu Ala Phe Glu Cys Ile Thr Gly Phe Arg Pro Phe Leu Pro
    210                 215                 220
Asn Trp Gln Pro Val Gln Trp His Ser Lys Val Arg Gln Lys Ser Glu
225                 230                 235                 240
Val Asp Ile Val Val Ser Glu Asp Leu Asn Gly Thr Val Lys Phe Ser
                245                 250                 255
Ser Ser Ser Pro Phe Pro Asn Asn Leu Asn Ser Val Leu Ala Glu Arg
            260                 265                 270
Leu Glu Lys Trp Leu Gln Leu Met Leu Thr Trp Gln Pro Arg Gln Arg
```

```
        275                 280                 285
Gly Val Asp Pro Gln Tyr Gly Pro Asn Gly Cys Phe Arg Ala Leu Asp
    290                 295                 300
Asp Ile Leu Asn Leu Lys Leu Val His Ile Leu Asn Met Val Thr Gly
305                 310                 315                 320
Thr Ile His Thr Tyr Pro Val Met Glu Asp Glu Ser Leu Gln Ser Leu
                325                 330                 335
Lys Thr Arg Ile Arg Glu Asp Thr Gly Ile Leu Glu Thr Asp Gln Glu
            340                 345                 350
Leu Leu Gln Glu Ala Gly Leu Val Leu Leu Pro Asp Lys Pro Ala Thr
        355                 360                 365
Gln Cys Ile Ser Asp Ser Lys Thr Asn Glu Gly
    370                 375
```

<210> 3
<211> 349
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence of p38 and ikk

<221> VARIANT
<222> (26)...(26)
<223> Phe or Tyr

<221> VARIANT
<222> (41)...(41)
<223> Ile or Val

<221> VARIANT
<222> (43)...(43)
<223> Ile or Val

<221> VARIANT
<222> (65)...(65)
<223> Met or Leu

<221> VARIANT
<222> (68)...(68)
<223> Met or Leu

<221> VARIANT
<222> (74)...(74)
<223> Ile or Val

<221> VARIANT
<222> (105)...(105)
<223> Asn or Gln

<221> VARIANT
<222> (114)...(114)
<223> Asp or Glu

<221> VARIANT
<222> (117)...(117)

<223> Ile of Val

<221> VARIANT
<222> (123)...(123)
<223> Asn or Gln

<221> VARIANT
<222> (149)...(149)
<223> Asn or Gln

<221> VARIANT
<222> (167)...(167)
<223> Asp or Gln

<221> VARIANT
<222> (172)...(172)
<223> Phe or Tyr

<221> VARIANT
<222> (185)...(185)
<223> Asn or Glu

<221> VARIANT
<222> (216)...(216)
<223> Asp or Gln

<221> VARIANT
<222> (218)...(218)
<223> Ile or Val

<221> VARIANT
<222> (219)...(219)
<223> Asp or Gln

<221> VARIANT
<222> (234)...(234)
<223> Asn or Glu

<221> VARIANT
<222> (249)...(249)
<223> Asn or Gln

<221> VARIANT
<222> (261)...(261)
<223> Asn or Gln

<221> VARIANT
<222> (267)...(267)
<223> Asn or Gln

<221> VARIANT
<222> (304)...(304)
<223> Asp or Glu

<221> VARIANT
<222> (325)...(325)
<223> Asp or Glu

<221> VARIANT
<222> (335)...(335)
<223> Ile or Val

<221> VARIANT
<222> (348)...(348)
<223> Asp or Glu

<400> 3

```
Met Gln Glu Arg Pro Ser Leu Pro Arg Gln Glu Cys Asn Ala Trp Glu
 1               5                  10                  15
Met Lys Glu Arg Leu Gly Ser Gly Ala Xaa Gly Asn Val Cys Ala Ala
            20                  25                  30
His Asx Gln Lys Thr Gly Glu Arg Xaa Ala Xaa Lys Gln Cys Arg Arg
        35                  40                  45
Glu Leu Ser Ile Ile Asn Ala Asp Arg Thr Cys Arg Glu Ile Arg Ile
    50                  55                  60
Xaa Arg Arg Xaa Asn His Glu Asn Val Xaa Ala Ala Arg Asp Val Phe
65                  70                  75                  80
Glu Gly Ala Arg Asn Leu Ala Glu Asn Asx Asp Leu Leu Ala Met Glu
                85                  90                  95
His Cys Gln Gly Ala Asp Leu Asn Xaa Ile Glu Asn Cys Cys Gly Leu
            100                 105                 110
Arg Xaa Asp Ala Xaa Gln Phe Leu Ile Ser Xaa Ile Ala Arg Ala Leu
        115                 120                 125
Arg Tyr Ile His Glu Ala Arg Ile Ile His Arg Asp Leu Lys Pro Glu
    130                 135                 140
Asn Ile Ala Leu Xaa Glx Asp Cys Glu Arg Lys Ile Ile Asp Leu Gly
145                 150                 155                 160
Leu Ala Arg Glu Leu Asp Xaa Glu Met Thr Gly Xaa Val Ala Thr Arg
                165                 170                 175
Gln Tyr Arg Ala Pro Glu Ile Leu Xaa Gln Gln His Tyr Asn Gln Thr
            180                 185                 190
Val Asp Ile Trp Ser Phe Gly Cys Ile Ala Ala Glu Cys Ile Thr Gly
        195                 200                 205
Arg Pro Leu Leu Pro Asn Thr Xaa His Xaa Xaa Arg Gln Lys Leu Glu
    210                 215                 220
Leu Arg Ile Val Gly Ser Glu Asp Ala Xaa Gly Leu Lys Lys Ile Ser
225                 230                 235                 240
Ser Glu Ser Ala Arg Asn Asn Ile Xaa Ser Leu Ala Ala Glu Arg Leu
                245                 250                 255
Glu Asn Phe Ala Xaa Leu Met Ile Gly Ala Xaa Pro Arg Ala Arg Asp
            260                 265                 270
Leu Asp Glu Gln Met Arg Ala Leu Asp Asp Asp Leu Arg Ile Lys Ala
        275                 280                 285
Ala Gln Ala Leu Ala His Ala Thr Ile Ala Gln Tyr His Asp Met Xaa
    290                 295                 300
Asp Glu Pro Leu Ala Asp Leu Lys Asp Arg Ile Arg Glu Asp Arg Asp
305                 310                 315                 320
Ile Leu Glu Asp Xaa Gln Glu Leu Leu Gln Glu Ala Glu Leu Xaa Leu
                325                 330                 335
Leu Pro Asp Lys Pro Ala Asp Gln Cys Glu Met Xaa Ser
            340                 345
```

<210> 4

<211> 393
<212> PRT
<213> Rattus norvegicus

<308> Q01986
<309> 1993-05-13

<400> 4

```
Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp
 1               5                  10                  15
Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala
            20                  25                  30
Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys
        35                  40                  45
Arg Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys
    50                  55                  60
Asp Asp Asp Phe Glu Lys Ile Ser Glu Leu Gly Ala Gly Asn Gly Gly
65                  70                  75                  80
Val Val Phe Lys Val Ser His Lys Pro Ser Gly Leu Val Met Ala Arg
                85                  90                  95
Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn Gln Ile Ile
            100                 105                 110
Arg Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro Tyr Ile Val Gly
        115                 120                 125
Phe Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser Ile Cys Met Glu
    130                 135                 140
His Met Asp Gly Gly Ser Leu Asp Gln Val Leu Lys Lys Ala Gly Arg
145                 150                 155                 160
Ile Pro Glu Gln Ile Leu Gly Lys Val Ser Ile Ala Val Ile Lys Gly
                165                 170                 175
Leu Thr Tyr Leu Arg Glu Lys His Lys Ile Met His Arg Asp Val Lys
            180                 185                 190
Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys Leu Cys Asp
        195                 200                 205
Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn Ser Phe Val
    210                 215                 220
Gly Thr Arg Ser Tyr Met Ser Pro Glu Arg Leu Gln Gly Thr His Tyr
225                 230                 235                 240
Ser Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser Leu Val Glu Met
                245                 250                 255
Ala Val Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys Glu Leu Glu
            260                 265                 270
Leu Leu Phe Gly Cys Gln Val Glu Gly Asp Ala Ala Glu Thr Pro Pro
        275                 280                 285
Arg Pro Arg Thr Pro Gly Arg Pro Leu Ser Ser Tyr Gly Met Asp Ser
    290                 295                 300
Arg Pro Pro Met Ala Ile Phe Glu Leu Leu Asp Tyr Ile Val Asn Glu
305                 310                 315                 320
Pro Pro Pro Lys Leu Pro Ser Gly Val Phe Ser Leu Glu Phe Gln Asp
                325                 330                 335
Phe Val Asn Lys Cys Leu Ile Lys Asn Pro Ala Glu Arg Ala Asp Leu
            340                 345                 350
Lys Gln Leu Met Val His Ala Phe Ile Lys Arg Ser Asp Ala Glu Glu
        355                 360                 365
Val Asp Phe Ala Gly Trp Leu Cys Ser Thr Ile Gly Leu Asn Gln Pro
    370                 375                 380
Ser Thr Pro Thr His Ala Ala Ser Ile
```

385 390

<210> 5
<211> 345
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence of p38 and MEK-1

<221> VARIANT
<222> (9)...(9)
<223> Phe or Tyr

<221> VARIANT
<222> (14)...(14)
<223> Asn or Gln

<221> VARIANT
<222> (22)...(22)
<223> Asp or Glu

<221> VARIANT
<222> (24)...(24)
<223> Phe or Tyr

<221> VARIANT
<222> (82)...(83)
<223> Ile or Val

<221> VARIANT
<222> (102)...(102)
<223> Leu or Met

<221> VARIANT
<222> (109)...(109)
<223> Asn or Gln

<221> VARIANT
<222> (110)...(110)
<223> Ile or Val

<221> VARIANT
<222> (118)...(118)
<223> Asp or Glu

<221> VARIANT
<222> (119)...(119)
<223> Asp or Gln

<221> VARIANT
<222> (128)...(128)
<223> Ile or Val

<221> VARIANT
<222> (176)...(176)

<223> Phe or Tyr

<221> VARIANT
<222> (189)...(189)
<223> Asn or Gln

<221> VARIANT
<222> (206)...(206)
<223> Leu or Met

<221> VARIANT
<222> (209)...(209)
<223> Leu or Met

<221> VARIANT
<222> (223)...(223)
<223> Asp or Glu

<221> VARIANT
<222> (255)...(255)
<223> Leu or Met

<221> VARIANT
<222> (285)...(285)
<223> Asp or Glu

<221> VARIANT
<222> (287)...(287)
<223> Asp or Gln

<221> VARIANT
<222> (290)...(290)
<223> Ile or Val

<221> VARIANT
<222> (303)...(303)
<223> Asp or Gln

<221> VARIANT
<222> (312)...(312)
<223> Phe or Tyr

<221> VARIANT
<222> (317)...(317)
<223> Asp or Glu

<221> VARIANT
<222> (320)...(320)
<223> Asp or Glu

<400> 5

```
Gln Gln Arg Glu Arg Leu Glu Ala Xaa Arg Gln Glx Leu Xaa Lys Thr
 1               5                  10                  15
Gly Glu Glu Lys Asp Xaa Arg Xaa Glx Asn Ile Ser Glu Leu Gly Ala
            20                  25                  30
Gly Ala Gly Gly Ser Val Cys Ala Ala Phe Asp Lys Lys Ser Gly His
        35                  40                  45
```

```
Arg Met Ala Arg Lys Leu Ile His Arg Glu Ile Gln Pro Ala Ile Arg
    50                  55                  60
Asn Arg Ile Ile Arg Glu Leu Arg Leu Leu His Glu Cys Asn His Glu
65                  70                  75                  80
Asn Xaa Xaa Gly Leu Leu Asp Ala Phe Thr Pro Ala Arg Glu Ile Glu
                85                  90                  95
Ile Cys Met Glu His Xaa Asp Gly Ala Asp Leu Asx Xaa Xaa Leu Lys
            100                 105                 110
Ala Gln Arg Ile Pro Xaa Xaa His Leu Gln Lys Leu Ile Ile Ala Xaa
        115                 120                 125
Ile Arg Gly Leu Lys Tyr Ile Arg Glu Ala Asp Ile Ile His Arg Asp
    130                 135                 140
Leu Lys Pro Ser Asn Ile Ala Val Asn Glu Arg Cys Glu Ile Lys Ile
145                 150                 155                 160
Cys Asp Phe Gly Leu Ala Arg Gln Leu Asp Asp Glu Met Ala Asn Xaa
                165                 170                 175
Val Ala Thr Arg Ser Tyr Arg Ala Pro Glu Arg Leu Xaa Gly Met His
            180                 185                 190
Tyr Asn Gln Gln Ser Asp Ile Trp Ser Met Gly Cys Ile Xaa Ala Glu
        195                 200                 205
Xaa Ala Thr Gly Arg Thr Leu Ile Pro Gly Pro Asp Ala Ile Xaa Gln
    210                 215                 220
Glu Leu Leu Ile Gly Arg Gln Val Glu Gly Asp Ala Ala Glu Leu Leu
225                 230                 235                 240
Lys Arg Ile Arg Ser Glu Gly Ala Arg Asn Ser Ile Gln Gly Xaa Ala
                245                 250                 255
Gln Arg Pro Lys Met Ala Phe Ala Asn Leu Asp Ile Gly Ala Asn Glu
            260                 265                 270
Leu Ala Pro Asp Leu Leu Glu Gly Met Leu Ser Leu Xaa Phe Xaa Asp
        275                 280                 285
Arg Xaa Asn Ala Ala Gln Ala Leu Ala His Ala Glu Arg Ala Xaa Leu
    290                 295                 300
His Glx Leu Met Ala Asp Ala Xaa Asp Gln Arg Phe Xaa Ala Arg Xaa
305                 310                 315                 320
Leu Asp Ile Ala Glu Trp Leu Cys Leu Thr Ile Asp Glu Asn Gln Pro
                325                 330                 335
Phe Thr Pro Pro His Ala Ala Gln Glu
            340                 345
```

<210> 6
<211> 18
<212> PRT
<213> Mus musculus

<308> BAA85877
<309> 1999-10-29

<400> 6

```
Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile Val Cys Ala
 1               5                  10                  15
Ala Tyr
```

<210> 7
<211> 23

<212> PRT
<213> Homo sapiens

<308> 18158777
<309> 2001-01-29

<400> 7
Gln Glu Val Ser Tyr Thr Asp Thr Lys Val Ile Gly Asn Gly Ser Phe
 1   5   10   15
Gly Val Val Tyr Gln Ala Lys
            20

<210> 8
<211> 18
<212> PRT
<213> Rattus norvegicus

<308> P47197
<309> 1996-06-01

<400> 8
Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile Leu
 1   5   10   15
Val Arg

<210> 9
<211> 24
<212> PRT
<213> Neurospora crassa

<308> T18359
<309> 1994-04-21

<400> 9
Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr
 1   5   10   15
Gln Val Arg Glu Ile Ala Lys Val
            20

<210> 10
<211> 15
<212> PRT
<213> Mus musculus

<308> BAA85877
<309> 1999-10-29

<400> 10
Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys
 1   5   10   15

<210> 11

<211> 13
<212> PRT
<213> Homo sapiens

<308> 18158777
<309> 2001-01-29

<400> 11
Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met Arg Lys
 1   5   10

<210> 12
<211> 15
<212> PRT
<213> Rattus norvegicus

<308> P47197
<309> 1996-06-01

<400> 12
Asp Glu Val Ala His Thr Val Thr Glu Ser Arg Val Leu Gln Asn
 1   5   10   15

<210> 13
<211> 24
<212> PRT
<213> Neurospora crassa

<308> T18359
<309> 1994-04-21

<400> 13
Leu Asp Leu Lys Asn Thr Ile Asn Thr Met Val Asp Arg Leu Gly Thr
 1   5   10   15
Phe Ala Phe Glu Val Ser Lys Val
            20

<210> 14
<211> 8
<212> PRT
<213> Mus musculus

<308> BAA85877
<309> 1999-10-29

<400> 14
Val Asn His Lys Asn Ile Ile Ser
 1   5

<210> 15
<211> 8
<212> PRT
<213> Homo sapiens

<308> 18158777
<309> 2001-01-29

<400> 15
Leu Asp His Cys Asn Ile Val Arg
 1   5

<210> 16
<211> 8
<212> PRT
<213> Rattus norvegicus

<308> P47197
<309> 1996-06-01

<400> 16
Thr Arg His Pro Phe Leu Thr Ala
 1   5

<210> 17
<211> 8
<212> PRT
<213> Neurospora crassa

<308> T18359
<309> 1994-04-21

<400> 17
Ala Arg Glu Val Gly Thr Asp Gly
 1   5

<210> 18
<211> 16
<212> PRT
<213> Mus musculus

<308> BAA85877
<309> 1999-10-29

<400> 18
Gln Asp Val Tyr Leu Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln
 1   5   10   15

<210> 19
<211> 16
<212> PRT
<213> Homo sapiens

<308> 18158777
<309> 2001-01-29

<400> 19

Val Tyr Leu Asn Leu Val Leu Asp Tyr Val Pro Glu Thr Val Tyr Arg
1 5 10 15

<210> 20
<211> 15
<212> PRT
<213> Rattus norvegicus

<308> P47197
<309> 1996-06-01

<400> 20
Cys Phe Val Met Glu Tyr Ala Asn Gly Gly Asp Leu Phe Phe His
1 5 10 15

<210> 21
<211> 16
<212> PRT
<213> Neurospora crassa

<308> T18359
<309> 1994-04-21

<400> 21
Lys Asp Leu Thr Glu Asn Val Asn Thr Met Ala Ser Asn Leu Thr Ser
1 5 10 15

<210> 22
<211> 5
<212> PRT
<213> Mus musculus

<308> BAA85877
<309> 1999-10-29

<400> 22
Val Met Asn Ser Glu
1 5

<210> 23
<211> 12
<212> PRT
<213> Homo sapiens

<308> 18158777
<309> 2001-01-29

<400> 23
Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile Gln
1 5 10

<210> 24

<211> 12
<212> PRT
<213> Rattus norvegicus

<308> P47197
<309> 1996-06-01

<400> 24
Leu Asp Gln Arg Thr His Phe Pro Gln Phe Ser Tyr
 1   5   10

<210> 25
<211> 12
<212> PRT
<213> Neurospora crassa

<308> T18359
<309> 1994-04-21

<400> 25
Val Phe Asn Ala Leu Lys Thr Leu Ala Val Lys Glu
 1   5   10

<210> 26
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> IKKb/p38 ATP chimera binding site

<400> 26
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1   5   10   15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20   25   30
Gly Ala Phe Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35   40   45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50   55   60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Met Lys His Met Lys His
65   70   75   80
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85   90   95
Glu Glu Phe Asn Asp Val Tyr Leu Val Glu His Leu Met Gly Ala Asp
            100   105   110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115   120   125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130   135   140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145   150   155   160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165   170   175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro
            340                 345                 350
Leu Asp Gln Glu Glu Met Glu Ser
        355                 360
```

<210> 27
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> MEK1/p38 ATP chimera binding site

<400> 27

```
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Gly Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His
65                  70                  75                  80
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Glu His Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro
            340                 345                 350
Leu Asp Gln Glu Glu Met Glu Ser
        355                 360
```

<210> 28
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> JNK-3/p38 ATP chimera binding site

<400> 28

```
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Gln Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Met Lys His Met Lys His
65                  70                  75                  80
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Met His Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro
            340                 345                 350
Leu Asp Gln Glu Glu Met Glu Ser
        355                 360
```

<210> 29
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> GSK-3/p38 ATP chimera binding site

<400> 29

```
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Phe Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Met Lys His Met Lys His
65                  70                  75                  80
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Leu His Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro
            340                 345                 350
Leu Asp Gln Glu Glu Met Glu Ser
        355                 360
```

<210> 30
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> Akt/p38 ATP chimera binding site

<400> 30

```
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Phe Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His
65                  70                  75                  80
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Glu His Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro
            340                 345                 350
Leu Asp Gln Glu Glu Met Glu Ser
        355                 360
```

<210> 31
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> NIK/p38 ATP chimera binding site

<400> 31

```
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Ala Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Ser Lys His Met Lys His
65                  70                  75                  80
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Val His Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro
            340                 345                 350
Leu Asp Gln Glu Glu Met Glu Ser
        355                 360


<210> 32
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> IKKb/p38 inhibitor binding site chimera

<400> 32
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Asn His
65                  70                  75                  80
Pro Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Thr Tyr Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Lys Pro
            340                 345                 350
Ala Thr Gln Cys Glu Met Glu Ser
        355                 360
```

<210> 33
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> MEK1/p38 inhibitor binding site chimera

<400> 33

```
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Asn His
65                  70                  75                  80
Pro Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Thr His
            340                 345                 350
Ala Ala Ser Ile Glu Met Glu Ser
        355                 360
```

<210> 34
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> JNK-3/p38 inhibitor binding site chimera

<400> 34

```
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Asn His
65                  70                  75                  80
Lys Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Thr Glu Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro
            340                 345                 350
Leu Asp Gln Glu Glu Met Glu Ser
        355                 360


<210> 35
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> GSK-3/p38 inhibitor binding site chimera

<400> 35
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Asp His
65                  70                  75                  80
Cys Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Thr Asp Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro His
            340                 345                 350
Ala Arg Ile Gln Glu Met Glu Ser
        355                 360
```

<210> 36
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> Akt/p38 inhibitor binding site chimera

<400> 36

```
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Arg His
65                  70                  75                  80
Pro Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Thr Tyr Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Phe Pro
            340                 345                 350
Gln Phe Ser Val Glu Met Glu Ser
        355                 360


<210> 37
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> NIK/p38 inhibitor binding site chimera

<400> 37
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Arg His
65                  70                  75                  80
Val Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Thr Asn Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Thr Leu
            340                 345                 350
Ala Val Lys Glu Glu Met Glu Ser
        355                 360
```

<210> 38
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> IKKb/p38 chimera

<400> 38

```
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His
65                  70                  75                  80
Pro Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Thr Tyr Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
            180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro
            340                 345                 350
Ala Asp Gln Glu Glu Met Glu Ser
        355                 360
```

<210> 39
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> JNK/p38 chimera

<400> 39

```
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1               5                  10                  15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
            20                  25                  30
Gly Ala Gln Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
        35                  40                  45
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
    50                  55                  60
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Met Lys His Met Lys His
65                  70                  75                  80
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
                85                  90                  95
Glu Glu Phe Asn Asp Val Tyr Leu Val Met Glu Leu Met Gly Ala Asp
            100                 105                 110
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
        115                 120                 125
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
    130                 135                 140
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145                 150                 155                 160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
                165                 170                 175
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
```

```
                180                 185                 190
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
        195                 200                 205
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
    210                 215                 220
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
225                 230                 235                 240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
                245                 250                 255
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn
            260                 265                 270
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met
        275                 280                 285
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala
    290                 295                 300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala
305                 310                 315                 320
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu
                325                 330                 335
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro
            340                 345                 350
Leu Asp Gln Glu Glu Met Glu Ser
        355                 360
```